

Microbial Source Tracking: The Application of a DNA-Based Molecular Approach to Identify Sources of Fecal Contamination in Region 4

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Microbial Source Tracking (MST) is a relatively novel approach that is considered to be the best tool available for identifying sources of fecal contamination in water. It is based on the assumption that specific strains of bacteria are associated with specific host species. Until recently, MST was primarily determined by comparing the phenotypic (biochemical) characteristics of bacterial indicator organisms. However, with the advent of molecular (genotypic) biology, DNA-based methods are showing great promise in offering the most precise identification of specific types of sources. Many in the scientific community feel that MST should be an integral part of any project that involves TMDL development for pathogens, and the design and implementation of Best Management Practices to reduce fecal loading in water. Several states have either entered into contracts with scientists at local universities or explored the feasibility of hiring commercial laboratories to analyze their impaired waters using MST methodologies, as a precursor to TMDL development. In the near future, it will become necessary for Regional Laboratories to develop technical competency in the area of MST in order to provide Regional Programs, states and stakeholders with reliable means to interpret and utilize information provided through Microbial Source Tracking. Through participation in the first EPA, Office of Research and Development, Regional Research Partnership Program, the Science and Ecosystem Support Division of Region 4 is developing technical competency in this area.

This study explores the utility of a DNA-based molecular approach, using Polymerase Chain Reaction (PCR)/Agarose Gel Electrophoresis, to identify species of enterococci bacteria isolated from cattle manure and streams in the Broad River watershed, located near Athens, Georgia. The Broad River is an impaired water body, impacted by human and animal fecal contamination, attributed primarily to septic tank systems and agricultural runoff. A library of isolates, obtained during the study, will be used in a multi-investigator study to address the utility and effectiveness of alternative bacterial indicators of fecal contamination, and the application of fairly new DNA-based technology, Amplified Fragment Length Polymorphisms (AFLP), to address the causes of impairment of surface waters when fecal contamination has been identified.